SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANTS: Ji, Hongjun
              Rosen, Craig A.

  (ii) TITLE OF INVENTION: Breast Cancer Specific Gene 1

 (iii) NUMBER OF SEQUENCES: 12

  (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
      (B) STREET: 1100 New York Ave., Suite 600
      (C) CITY: Washington
      (D) STATE: DC
      (E) COUNTRY: USA
      (F) ZIP: 20005-3934

   (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: US 09/017,715
      (B) FILING DATE: 1998-FEB-03
      (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: US 08/673,284
      (B) FILING DATE: 28-JUN-96
      (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: US 60/000,602
      (B) FILING DATE: 30-JUN-95
      (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: PCT/US95/08295
      (B) FILING DATE: 30-JUN-95
      (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: US 60/037,080
      (B) FILING DATE: 03-FEB-97
      (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Steffe, Eric K.
      (B) REGISTRATION NUMBER: 36,688
      (C) REFERENCE/DOCKET NUMBER: 1488.0810003

  (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: 202-371-2600
      (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

     (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 550 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: both

    (ii) MOLECULE TYPE: cDNA

    (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION: 12..392

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CACGAGCCAC C ATG GAT GTT TTC AAG AAG GGC TTC TCC ATC GCC AAG AAG        50
           Met Asp Val Phe Lys Lys Gly Phe Ser Ile Ala Lys Lys
            1             5                  10

GGC GTG GTG GGT GCG GTG GAA AAG ACC AAG CAG GGG GTG ACG GAA GCA        98
Gly Val Val Gly Ala Val Glu Lys Thr Lys Gln Gly Val Thr Glu Ala
    15              20                  25

GCT GAG AAG ACC AAG GAG GGG GTC ATG TAT GTG GGA GCC AAG ACC AAG        146
Ala Glu Lys Thr Lys Glu Gly Val Met Tyr Val Gly Ala Lys Thr Lys
30              35                  40                      45

GAG AAT GTT GTA CAG AGC GTG ACC TCA GTG GCC GAG AAG ACC AAG GAG        194
Glu Asn Val Val Gln Ser Val Thr Ser Val Ala Glu Lys Thr Lys Glu
            50                  55                  60

CAG GCC AAC GCC GTG AGC AAG GCT GTG GTG AGC AGC GTC AAC ACT GTG        242
Gln Ala Asn Ala Val Ser Lys Ala Val Val Ser Ser Val Asn Thr Val
        65                  70                  75

GCC ACC AAG ACC GTG GAG GAG GCG GAG AAC ATC GCG GTC ACC TCC GGG        290
Ala Thr Lys Thr Val Glu Glu Ala Glu Asn Ile Ala Val Thr Ser Gly
        80                  85                  90

GTG GTG CGC AAG GAG GAC TTG AGG CCA TCT GCC CCC CAA CAG GAG GGT        338
Val Val Arg Lys Glu Asp Leu Arg Pro Ser Ala Pro Gln Gln Glu Gly
    95                  100                 105

GAG GCA TCC AAA GAG AAA GAG GAA GTG GCA GAG GAG GCC CAG AGT GGG        386
Glu Ala Ser Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly
110                 115                 120                 125

GGA GAC TAGAGGGCTA CAGGCCAGCG TGGATGACCT GAAGAGCGCT CCTCTGCCTT        442
Gly Asp


GGACACCATC CCCTCCTAGC ACAAGGAGTG CCCGCCTTGA GTGACATGCG GGTGCCCACG        502

CTCCTGCCCT CGTCTCCCTG GACACCCTTG GCCTGTCCAC CTGTGCTG                     550
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(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 127 amino acids
            (B) TYPE: amino acid

          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Val Phe Lys Lys Gly Phe Ser Ile Ala Lys Lys Gly Val Val
 1   5   10   15

Gly Ala Val Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
                20   25   30

Thr Lys Glu Gly Val Met Tyr Val Gly Ala Lys Thr Lys Glu Asn Val
        35   40   45

Val Gln Ser Val Thr Ser Val Ala Glu Lys Thr Lys Glu Gln Ala Asn
    50   55   60

Ala Val Ser Lys Ala Val Val Ser Ser Val Asn Thr Val Ala Thr Lys
65   70   75   80

Thr Val Glu Glu Ala Glu Asn Ile Ala Val Thr Ser Gly Val Val Arg
                85   90   95

Lys Glu Asp Leu Arg Pro Ser Ala Pro Gln Gln Glu Gly Glu Ala Ser
            100   105   110

Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly Gly Asp
        115   120   125

(2) INFORMATION FOR SEQ ID NO:3:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: cDNA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGGATCCAT GTTTTCAAGA AGG   23

(2) INFORMATION FOR SEQ ID NO:4:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: cDNA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAAGCTTCT AGTCTCCCCC ACTCTGG   27

(2) INFORMATION FOR SEQ ID NO:5:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 25 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGGATCCCG ATGTTTTCAA GAAGG   25

(2) INFORMATION FOR SEQ ID NO:6:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 27 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGTACCCT AGTCTCCCCC ACTCTGG   27

(2) INFORMATION FOR SEQ ID NO:7:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 29 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGGATCCGC CACCATGTTT TCAAGAAGG   29

(2) INFORMATION FOR SEQ ID NO:8:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 60 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGGATCCTC AGAAAGCGTA GTCTGGGACG TCGTATGGGT ACTAGTCTCC CCCACTCTGG   60

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGTACCTC ACTAGTCTCC CCCACTCTGG   30

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3974 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: both

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT   60

GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG   120

CCGGAAGCAT AAAGTGTAAA GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG   180

CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA   240

TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA   300

CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG   360

TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC   420

AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC   480

CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CGACAGGAC   540

TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC   600

TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA   660

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GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC    720

ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA    780

ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG    840

CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA    900

GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG    960

GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC   1020

AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT   1080

CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA   1140

CAATTCGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA   1200

ACCTTTCGCG GTATGGCATG ATAGCGCCCG AAGAGAGTC AATTCAGGGT GGTGAATGTG   1260

AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTTCC   1320

CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG   1380

ATGGCGGAGC TGAATTACAT TCCCAACCGC GTGGCACAAC AACTGGCGGG CAAACAGTCG   1440

TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTCGCG   1500

GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTCGAT GGTAGAACGA   1560

AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG   1620

CTGATCATTA ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT   1680

AATGTTCCGG CGTTATTTCT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC   1740

TCCCATGAAG ACGGTACGCG ACTGGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA   1800

ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGGCGC GTCTGCGTCT GGCTGGCTGG   1860

CATAAATATC TCACTCGCAA TCAAATTCAG CCGATAGCGG AACGGGAAGG CGACTGGAGT   1920

GCCATGTCCG GTTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCACTGCG   1980

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CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT   2100

TATATCCCGC CGTTAACCAC CATCAAACAG GATTTTCGCC TGCTGGGGCA AACCAGCGTG   2160

GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG CAATCAGCT GTTGCCCGTC   2220

TCACTGGTGA AAAGAAAAAC CACCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG   2280

TTGGCCGATT CATTAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA   2340

GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTCGACC AAAGCGGCCA TCGTGCCTCC   2400

CCACTCCTGC AGTTCGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC   2460

GACGGATTTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA   2520
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CCAACTCGCG AGGGGATCGA GCCCGGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG    2580

CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA    2640

GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGGC GTCGCTTGGT CGGTCATTTC    2700

GAACCCCAGA GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC    2760

GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTC GCCGCCAAGC    2820

TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC    2880

CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG    2940

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AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA    3060

CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG    3120

CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC    3180

TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC    3240

CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG    3300

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TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT    3600

TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT    3660

GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT    3720

CTCTTTGCGC TTGCGTTTTC CCTTGTCCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT    3780

CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC    3840

CCTGAGTGCT TGCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG    3900

CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTCACAC ATTAAAGAGG    3960

AGAAATTACA TATG                                                      3974
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(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 112 base pairs
       -(B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: both

    (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC   60

CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG   112

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 755 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCGCTGCGG CAGACTCGAG CCAGCTCAAG CCCGCAGCTC GCAGGGAGAT CCAGCTCCGT   60

CCTGCCTGCA GCAGCCAACC CTGCACACCC ACCATGGATG TTTCAAGAAG GGCTTCTCCA   120

TCGCCAAGGA GGGCGTGGTG GGTGCGGTGG AAAAGACCAA GCAGGGGGTG ACGGAAGCAG   180

CTGAGAAGAC CAAGGAGGGG GTCATGTATG TGGGAGCCAA GACCAAGGAG AATGTTGTAT   240

GTACAGAGCG TGACCTCAGT GGCCGAGAAG ACCAAGGAGC AGGCCAACGC CGTGAGCAAG   300

GCTGTGGTGA GCAGCGTCAA CACTTGGCCA CCAAGACCGT GAGGAGGCGG AGAACATCGC   360

GGTCACTCCG GGTGTGCGCA AGGAGGATTA GGCCATTCCC CCCAACAGGA GGGTGAGGCA   420

TCAAGAAGAG AAGGGCAGGC AGAGTGGGGG AGACTAGAGG CTACAGGCC AGCTTGGATG   480

ACCTGAAGAG CGCTCCTCTG CCTTGGGACA CCATCCCCTC CTAGCACAAG GAGTGCCCGC   540

TTTGAGTGGA CATGCGGCTG TCCCACGTTC CTGCCCTCGT TTTCCCTGGG CCACCTTGGC   600

CTGTCCAACT GTGCTGTTGC AACCAACTTA ATTGCCTTCC TTGGGCCCCA ACCAACTTTT   660

TGGTTCTTTT TGACCCATTT ATGTTTGTTG TGAATTTTTT TTTTAAAAGA TTTCAAATAA   720

AATTTGGGCC CATTTTTTAA AAAAAAAAA AAAAA   755

SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANTS: Ji, Hongjun
                   Rosen, Craig A.

  (ii) TITLE OF INVENTION: Breast Cancer Specific Gene 1

 (iii) NUMBER OF SEQUENCES: 11

  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
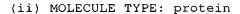   (B) STREET: 1100 New York Ave., Suite 600
     (C) CITY: Washington
     (D) STATE: DC
     (E) COUNTRY: USA
     (F) ZIP: 20005-3934

   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: TO BE ASSIGNED
     (B) FILING DATE: HEREWITH
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 08/673,284
     (B) FILING DATE: 28-JUN-96
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 60/000,602
     (B) FILING DATE: 30-JUN-95
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: PCT/US95/08295
     (B) FILING DATE: 30-JUN-95
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 60/037,080
     (B) FILING DATE: 03-FEB-97
     (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Steffe, Eric K.
     (B) REGISTRATION NUMBER: 36,688
     (C) REFERENCE/DOCKET NUMBER: 1488.0810003

  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: 202-371-2600
     (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

```
    (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 550 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: both

   (ii) MOLECULE TYPE: cDNA


   (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION: 12..392


   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
```

```
CACGAGCCAC C ATG GAT GTT TTC AAG AAG GGC TTC TCC ATC GCC AAG AAG        50
             Met Asp Val Phe Lys Lys Gly Phe Ser Ile Ala Lys Lys
              1               5                  10

GGC GTG GTG GGT GCG GTG GAA AAG ACC AAG CAG GGG GTG ACG GAA GCA        98
Gly Val Val Gly Ala Val Glu Lys Thr Lys Gln Gly Val Thr Glu Ala
 15                  20                  25

GCT GAG AAG ACC AAG GAG GGG GTC ATG TAT GTG GGA GCC AAG ACC AAG       146
Ala Glu Lys Thr Lys Glu Gly Val Met Tyr Val Gly Ala Lys Thr Lys
 30                  35                  40                  45

GAG AAT GTT GTA CAG AGC GTG ACC TCA GTG GCC GAG AAG ACC AAG GAG       194
Glu Asn Val Val Gln Ser Val Thr Ser Val Ala Glu Lys Thr Lys Glu
                 50                  55                  60

CAG GCC AAC GCC GTG AGC AAG GCT GTG GTG AGC AGC GTC AAC ACT GTG       242
Gln Ala Asn Ala Val Ser Lys Ala Val Val Ser Ser Val Asn Thr Val
                 65                  70                  75

GCC ACC AAG ACC GTG GAG GAG GCG GAG AAC ATC GCG GTC ACC TCC GGG       290
Ala Thr Lys Thr Val Glu Glu Ala Glu Asn Ile Ala Val Thr Ser Gly
                 80                  85                  90

GTG GTG CGC AAG GAG GAC TTG AGG CCA TCT GCC CCC CAA CAG GAG GGT       338
Val Val Arg Lys Glu Asp Leu Arg Pro Ser Ala Pro Gln Gln Glu Gly
     95                  100                 105

GAG GCA TCC AAA GAG AAA GAG GAA GTG GCA GAG GAG GCC CAG AGT GGG       386
Glu Ala Ser Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly
110                 115                 120                 125

GGA GAC TAGAGGGCTA CAGGCCAGCG TGGATGACCT GAAGAGCGCT CCTCTGCCTT       442
Gly Asp


GGACACCATC CCCTCCTAGC ACAAGGAGTG CCCGCCTTGA GTGACATGCG GGTGCCCACG      502

CTCCTGCCCT CGTCTCCCTG GACACCCTTG GCCTGTCCAC CTGTGCTG                   550


(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 127 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear
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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Asp Val Phe Lys Lys Gly Phe Ser Ile Ala Lys Lys Gly Val Val
 1               5                  10                 15

Gly Ala Val Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
             20                  25                 30

Thr Lys Glu Gly Val Met Tyr Val Gly Ala Lys Thr Lys Glu Asn Val
         35                  40                 45

Val Gln Ser Val Thr Ser Val Ala Glu Lys Thr Lys Glu Gln Ala Asn
     50                  55                 60

Ala Val Ser Lys Ala Val Val Ser Ser Val Asn Thr Val Ala Thr Lys
 65                  70                 75                 80

Thr Val Glu Glu Ala Glu Asn Ile Ala Val Thr Ser Gly Val Val Arg
             85                  90                 95

Lys Glu Asp Leu Arg Pro Ser Ala Pro Gln Gln Glu Gly Glu Ala Ser
             100                 105                110

Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly Gly Asp
         115                 120                 125
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(2) INFORMATION FOR SEQ ID NO:3:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 23 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGGATCCAT GTTTTCAAGA AGG   23

(2) INFORMATION FOR SEQ ID NO:4:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: cDNA

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAAGCTTCT AGTCTCCCCC ACTCTGG   27

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGGATCCCG ATGTTTTCAA GAAGG   25

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 27 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGTACCCT AGTCTCCCCC ACTCTGG   27

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 29 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGGATCCGC CACCATGTTT TCAAGAAGG   29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 60 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGGGATCCTC AGAAAGCGTA GTCTGGGACG TCGTATGGGT ACTAGTCTCC CCCACTCTGG   60

(2) INFORMATION FOR SEQ ID NO:9:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 30 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: cDNA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGGTACCTC ACTAGTCTCC CCCACTCTGG   30

(2) INFORMATION FOR SEQ ID NO:10:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 3974 base pairs
          (B) TYPE: nucleic acid,
          (C) STRANDEDNESS: both
          (D) TOPOLOGY: both

     (ii) MOLECULE TYPE: cDNA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTTGAAT TCGTAATCAT   60

GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG   120

CCGGAAGCAT AAAGTGTAAA GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG   180

CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA   240

TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG CTCTTCCGCT TCCTCGCTCA   300

CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG   360

TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC   420

AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTTCCAT AGGCTCCGCC   480

CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CGACAGGAC   540

TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC   600

TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA   660

GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC   720

ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA   780

ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG   840

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CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA      900

GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG      960

GTAGCTCTTG ATCCGGCAAA CAAACCACCG CTGGTAGCGG TGGTTTTTTT GTTTGCAAGC     1020

AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGGT     1080

CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCATGAGA TTATCGTCGA     1140

CAATTCGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTTG ACACCATCGA ATGGTGCAAA     1200

ACCTTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAGGGT GGTGAATGTG     1260

AAACCAGTAA CGTTATACGA TGTCGCAGAG TATGCCGGTG TCTCTTATCA GACCGTTTCC     1320

CGCGTGGTGA ACCAGGCCAG CCACGTTTCT GCGAAAACGC GGGAAAAAGT GGAAGCGGCG     1380

ATGGCGGAGC TGAATTACAT TCCCAACCGC GTGGCACAAC AACTGGCGGG CAAACAGTCG     1440

TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTCGCA AATTGTCGCG     1500

GCGATTAAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTCGAT GGTAGAACGA     1560

AGCGGCGTCG AAGCCTGTAA AGCGGCGGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG     1620

CTGATCATTA ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT     1680

AATGTTCCGG CGTTATTTCT TGATGTCTCT GACCAGACAC CCATCAACAG TATTATTTTC     1740

TCCCATGAAG ACGGTACGCG ACTGGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA     1800

ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGGCGC GTCTGCGTCT GGCTGGCTGG     1860

CATAAATATC TCACTCGCAA TCAAATTCAG CCGATAGCGG AACGGGAAGG CGACTGGAGT     1920

GCCATGTCCG GTTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCACTGCG     1980

ATGCTGGTTG CCAACGATCA GATGGCGCTG GGCGCAATGC GCGCCATTAC CGAGTCCGGG     2040

CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT     2100

TATATCCCGC CGTTAACCAC CATCAAACAG GATTTTCGCC TGCTGGGGCA AACCAGCGTG     2160

GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCCGTC     2220

TCACTGGTGA AAAGAAAAAC CACCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG     2280

TTGGCCGATT CATTAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA     2340

GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTCGACC AAAGCGGCCA TCGTGCCTCC     2400

CCACTCCTGC AGTTCGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTTT CCTGGATGCC     2460

GACGGATTTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA     2520

CCAACTCGCG AGGGGATCGA GCCCGGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG     2580

CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA     2640

GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGGC GTCGCTTGGT CGGTCATTTC     2700

GAACCCCAGA GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC     2760
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GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTC GCCGCCAAGC      2820

TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC      2880

CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG      2940

GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCGCGCCTT GAGCCTGGCG      3000

AACAGTTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA      3060

CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG      3120

CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC      3180

TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC      3240

CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG      3300

GCCAGCCACG ATAGCCGCGC TGCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTCG      3360

GTCTTGACAA AAAGAACCGG GCGCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG      3420

CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA      3480

GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA      3540

TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT      3600

TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT      3660

GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT      3720

CTCTTTGCGC TTGCGTTTTC CCTTGTCCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT      3780

CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC      3840

CCTGAGTGCT TGCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG      3900

CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTCACAC ATTAAAGAGG      3960

AGAAATTACA TATG                                                       3974
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(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 112 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: both

    (ii) MOLECULE TYPE: cDNA

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC        60

CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGAG AAATTACATA TG               112
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